# FIGURE 1



TTGGCGGGCGGAAGCGGCCACAACCCGGCGATCGAAAAGATTCTTAGGAACGCCGTACCA
GCCGCGTCTCTCAGGACAGCAGGCCCCTGTCCTTCTGTCGGGCGCCGCTCAGCCGTGCCC
TCCGCCCCTCAGGTTCTTTTTCTAATTCCAAATAAACTTGCAAGAGGACT**ATG**AAAGATT
ATGATGAACTTCTCAAATATTATGAATTACATGAAACTATTGGGACAGGTGGCTTTGCAA
AGGTCAAACTTGCCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAATCATGGATA
AAAACACACTAGGGAGTGATTTGCCCCGGATCAAAACGGAGATTGAGGCCTTGAAGAACC
TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGACAGCCAACAAAATATTCA
TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCCAGGATCGCC
TGTCAGAAGAGGAGACCCGGGTTGTCTTCCGTCAGATAGTATCTGCTGTTGCTTATGTGC
ACAGCCAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAATTTGCTGTTTGATGAATATC
ATAAATTAAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAAGGGTAACAAGGATTACC
ATCTACAGACATGCTGTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATACAAGGCAAAT
CATATCTTGGATCAGAGGCAGATGTTTGGAGCATGGGCATACTGTTATATGTTCTTATGT
GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAAGAAGATTATGAGAG
GAAAATATGATGTTCCCAAGTGGCTCTCTCCCAGTAGCATTCTGCTTCTTCAACAAATGC
TGCAGGTGGACCCAAAGAAACGGATTTCTATGAAAAATCTATTGAACCATCCCTGGATCA
TGCAAGATTACAACTATCCTGTTGAGTGGCAAAGCAAGAATCCTTTTATTCACCTCGATG
ATGATTGCGTAACAGAACTTTCTGTACATCACAGAAACAACAGGCAAACAATGGAGGATT
TAATTTCACTGTGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTTCTAGCCAAGA
AGGCTCGGGGAAAACCAGTTCGTTTAAGGCTTTCTTCTTTCTCCTGTGGACAAGCCAGTG
CTACCCCATTCACAGACATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGTG
ATAAAAATTATGTGGCGGGATTAATAGACTATGATTGGTGTGAAGATGATTTATCAACAG
GTGCTGCTACTCCCCGAACATCACAGTTTACCAAGTACTGGACAGAATCAAATGGGGTGG
AATCTAAATCATTAACTCCAGCCTTATGCAGAACACCTGCAAATAAATTAAAGAACAAAG
AAAATGTATATACTCCTAAGTCTGCTGTAAAGAATGAAGAGTACTTTATGTTTCCTGAGC
CAAAGACTCCAGTTAATAAGAACCAGCATAAGAGAGAAATACTCACTACGCCAAATCGTT
ACACTACACCCTCAAAAGCTAGAAACCAGTGCCTGAAAGAAACTCCAATTAAAATACCAG
TAAATTCAACAGGAACAGACAAGTTAATGACAGGTGTCATTAGCCCTGAGAGGCGGTGCC
GCTCAGTGGAATTGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAAGAAAGGGAG
CCAAAGTGTTTGGGAGCCTTGAAAGGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA
GCAAAAGGAAGGGTTCTGCCAGAGACGGGCCCAGAAGACTAAAGCTTCACTATAATGTGA
CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATTCTTCCAA
AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAACACAGTCAGATT
TTGGGAAAGTGACAATGCAATTTGAATTAGAAGTGTGCCAGCTTCAAAAACCCGATGTGG
TGGGTATCAGGAGGCAGCGGCTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGGAAG
ACATCCTATCTAGCTGCAAGGTA**TAA**TTGATGGATTCTTCCATCCTGCCGGATGAGTGTG
GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA
CTACCAACTTGTTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAAA
GATATTATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCATTATGTTACTGTCTTTTT
TAATCATGTGGTTTTGTATATTAATAATTGTTGACTTTCTTAGATTCACTTCCATATGTG
AATGTAAGCTCTTAACTATGTCTCTTTGTAATGTGTAATTTCTTTCTGAAATAAAACCAT
TTGTGAATAT

# FIGURE 2



MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA
LKNLRHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEEETRVVFRQIVSAV
AYVHSQGYAHRDLKPENLLFDEYHKLKLIDFGLCAKPKGNKDYHLQTCCGSLAYAAPELI
QGKSYLGSEADVWSMGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPKWLSPSSILLL
QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFIHLDDDCVTELSVHHRNNRQT
MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFSCGQASATPFTDIKSNNWSLEDV
TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL
KNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKREILTTPNRYTTPSKARNQCLKETPI
KIPVNSTGTDKLMTGVISPERRCRSVELDLNQAHMEETPKRKGAKVFGSLERGLDKVITV
LTRSKRKGSARDGPRRLKLHYNVTTTRLVNPDQLLNEIMSILPKKHVDFVQKGYTLKCQT
QSDFGKVTMQFELEVCQLQKPDVVGIRRQRLKGDAWVYKRLVEDILSSCKV

N-glycosylation site.

354-357
485-488
562-565

cAMP- and cGMP-dependent protein kinase phosphorylation site.

250-253
546-549

Tyrosine kinase phosphorylation site.

2-10
421-427
630-638

N-myristoylation site.

340-345

Microbodies C-terminal targeting signal.

649-652

Leucine zipper pattern.

165-186

Serine/Threonine protein kinases active-site signature.

128-140

Protein kinase domain

11-263

Kinase associated domain 1

602-651

# FIGURE 3



GTGCGATCCCGGGCCCGAGGGCATCAGACGGCGGCTGATTAGCTCCGGTTTGCATCACCC
GGACCGGGGGATTAGCTCCGGTTTGCATCACCCGGACCGGGGGCCGGGCGCGCACGAGAC
TCGCAGCGGAAGTGGAGGCGGCTCCGCGCGCGTCCGCTGCTAGGACCCGGGCAGGGCTGG
AGCTGGGCTGGGATCCCGAGCTCGGCAGCAGCGCAGCGGGCCGGCCCACCTGCTGGTGCC
CTGGAGGCTCTGAGCCCCGGCGGCGCCCGGGCCCACGCGGAACGACGGGGCGAG**ATG**CGA
GCCACCCCTCTAGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGAT
GACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGA
CTGCCCCCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTG
GCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGGGCGGGCC
TACCAGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAG
GAAGCCCCGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCCGCACAAGCATGTGGCTCGG
CCCACTGAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTTTCACTCGGACCCATGGG
GACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTC
TTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGAT
CTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTGGAGAAC
CTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGC
CCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCC
GATGTCTGGAGCCTGGGCGTGGCGCTCTTCACCATGCTGGCCGGCCACTACCCCTTCCAG
GACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCA
GGCCTCTCGGCCCCTGCCCGCTGTCTGGTTCGCTGCCTCCTTCGTCGGGAGCCAGCTGAA
CGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCTTA
GCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGTCTGGGGCTG
GACGAAGCCAGGGAAGAGGAGGGAGACAGAGAAGTGGTTCTGTATGGC**TAG**GACCACCCT
ACTACACGCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGTAGCTCCAAGCCTTCTCCTG
CCTCTGAACTGAGCCAAACCTTCAGTGCCTTCCAGAAGGGAGAAAGGCAGAAGCCTGTGT
GGAGTGTGCTGTGTACACATCTGCTTTGTTCCACACACATGCAGTTCCTGCTTGGGTGCT
TATCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAAT
ATTCCCTGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGAC
CATAGGTCACTGTCTACACTGGGTACACTTTGTACCAGTGTCGGCCTCCACTGATGCTGG
TGCTCAGGCACCTCTGTCCAAGGACAATCCCTTTCACAAACAAACCAGCTGCCTTTGTAT
CTTGTACCTTTTCAGAGAAAGGGAGGTATCCCTGTGCCAAAGGCTCCAGGCCTCTCCCCT
GCAACTCAGGACCCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCAGCATCTCTGTCCTC
TTGATTAAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCC
AAACTATGAGGCTAGTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTG
TCAACCATGGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTG
TCCTGTGGCCACCTGGAAAGTCCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAA
TCCCAGGTCCATACTCTAGGTTTTGGATACCATGAGTATGTATGTTTACCTGTGCCTAAT
AAAGGAGAATTATGAAATAAAAAAAAAAAAAAAAAA

# FIGURE 4



MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT
AVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCKVYPVQEAPAVLEPYARLPPHKHV
ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL
RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG

N-myristoylation site.

91-96
341-346

Protein kinase domain

71-315

# FIGURE 5



GAAGTTTCTCACTAGGGTCTTCTCTGGCCCAGCCTTTGACTGAAGCTGGTCTGGAGACAG
GGGCATTAGAGAAGTGACTCATAGATGGCCTAAAGAAGCGGGGCCACTCAAGGACCCAGG
ACAGAGGGAAGAGGGCCAACCCAGCTGGACCACAGGCAAACCCCATTGCCTTTGAGAGAA
AGAAGAGGACCCGGTGAAAC**ATG**CTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCG
TCTACGAGATCCGCGAGAGGCTCGGCTCGGGTGCCTTCTCCGAGGTGGTGCTGGCCCAGG
AGCGGGGCTCCGCACACCTCGTGGCCCTCAAGTGCATCCCCAAGAAGGCCCTCCGGGGCA
AGGAGGCCCTGGTGGAGAACGAGATCGCAGTGCTCCGTAGGATCAGTCACCCCAACATCG
TCGCTCTGGAGGATGTCCACGAGAGCCCTTCCCACCTCTACCTGGCCATGGAACTGGTGA
CGGGTGGCGAGCTGTTTGACCGCATCATGGAGCGCGGCTCCTACACAGAGAAGGATGCCA
GCCATCTGGTGGGTCAGGTCCTTGGCGCCGTCTCCTACCTGCACAGCCTGGGGATCGTGC
ACCGGGACCTCAAGCCCGAAAACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCA
TGGTCTCTGACTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTG
GGACCCCTGGATATGTGGCCCCAGAGCTCTTGGAGCAGAAACCCTACGGGAAGGCCGTAG
ATGTGTGGGCCCTGGGCGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCCTTCTACG
ACGAGAGCGACCCTGAGCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTXTC
CTTTCTGGGATGACATCTCAGAATCAGGCAAAGACTTTATTCGGCACCTTCTGGAGCGAG
ACCTTCAGAAGAGGTTCACCTGCCAACAGGCCTTGCGGGACCTTTGGATCTTTTGGGACA
CAGGCTTTGGCAGGGACATCTTAGGGTTTGTCAGTGAGCAGATCCGGAAGAACTTTGCTT
GGACACACTGGAAGCGAGCCTTCAATGCCACCTTGTTCCTGCGCCACATCCGGAAGCTGG
GGCAGATCCCAGAGGGCGAGGGGGCCTCTGAGCAGGGCATGGSCCGXCACAGCCACTXAG
GCCTTCGTGCTGGCCAGCCCCCCAAGTGG**TGA**TGCCCAGGXAGATGCCGAGGCCAAGTGG
AXTGAXCCCCAGATTTXCTTXC

# FIGURE 6



MLLLKKHTEDISSVYEIRERLGSGAFSEVVLAQERGSAHLVALKCIPKKALRGKEALVEN
EIAVLRRISHPNIVALEDVHESPSHLYLAMELVTGGELFDRIMERGSYTEKDASHLVGQV
LGAVSYLHSLGIVHRDLKPENLLYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTPGYVA
PELLEQKPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYEFDXPFWDDIS
ESGKDFIRHLLERDLQKRFTCQQALRDLWIFWDTGFGRDILGFVSEQIRKNFAWTHWKRA
FNATLFLRHIRKLGQIPEGEGASEQGMXRHSHXGLRAGQPPKW

N-glycosylation site.

302-305

cAMP- and cGMP-dependent protein kinase phosphorylation site.

5-8
66-69
257-260

Tyrosine kinase phosphorylation site.

101-108

N-myristoylation site.

118-123
166-171
170-175
334-339

Serine/Threonine protein kinases active-site signature.

132-144

Protein kinase domain

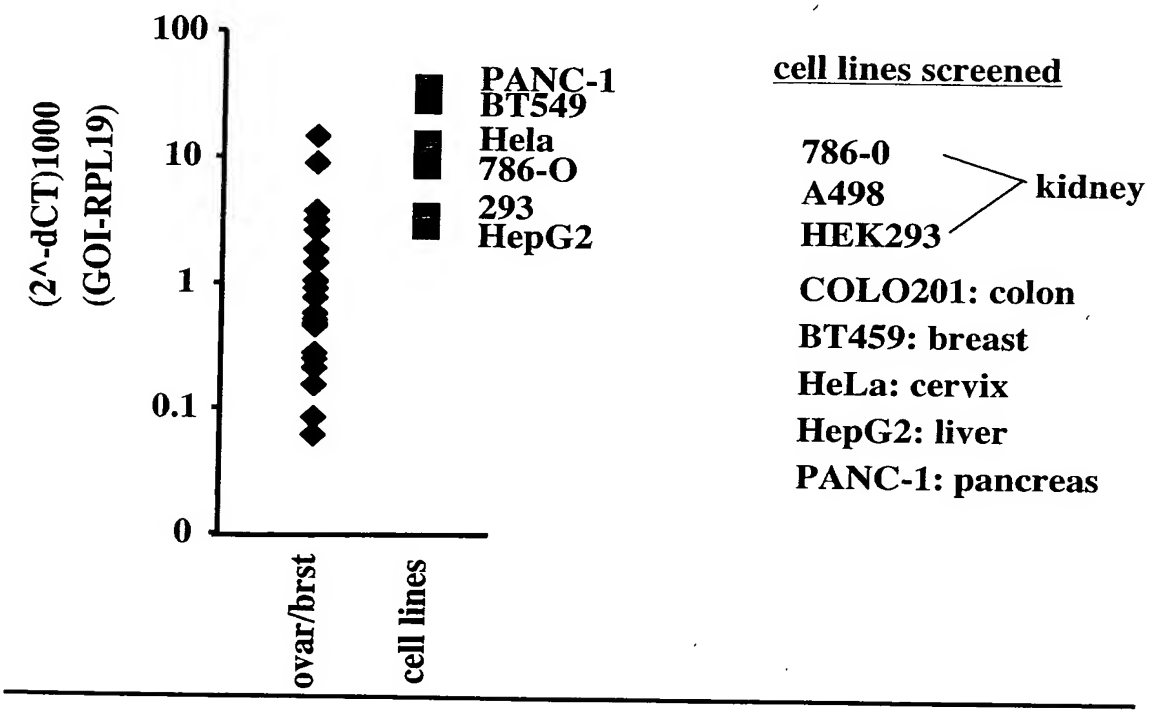
15-270

**FIGURE 7**



# TASK110 expression data

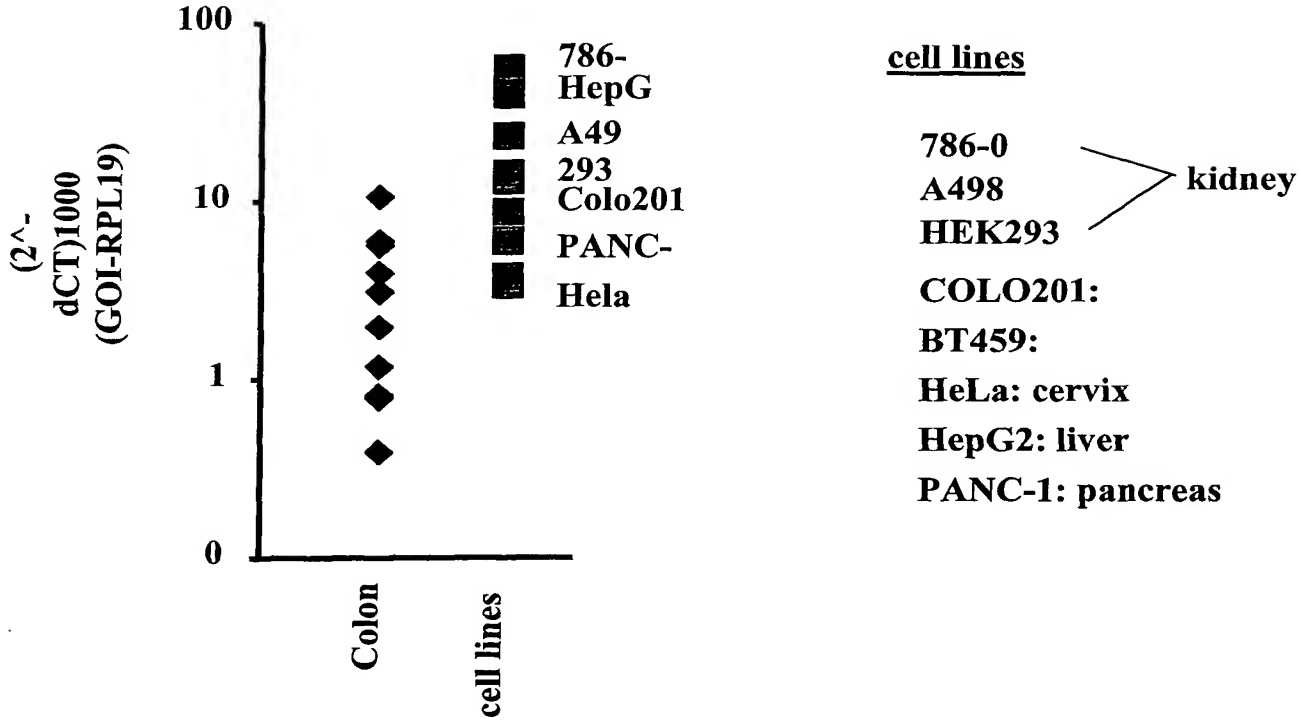
Tumor samples versus cell lines



# FIGURE 8



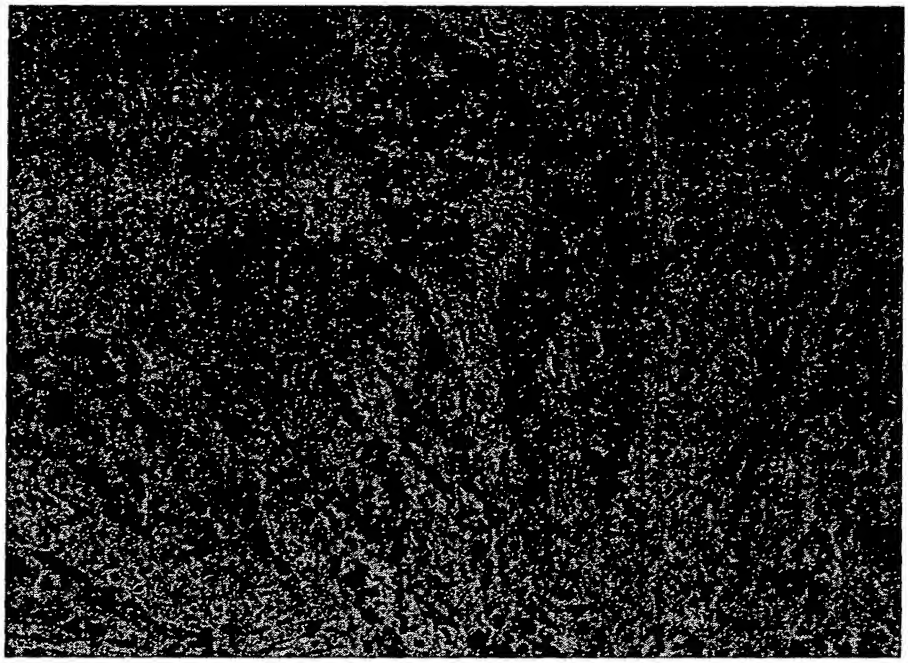
**TASK119 expression: tumor samples versus cell lines**



# FIGURE 9A



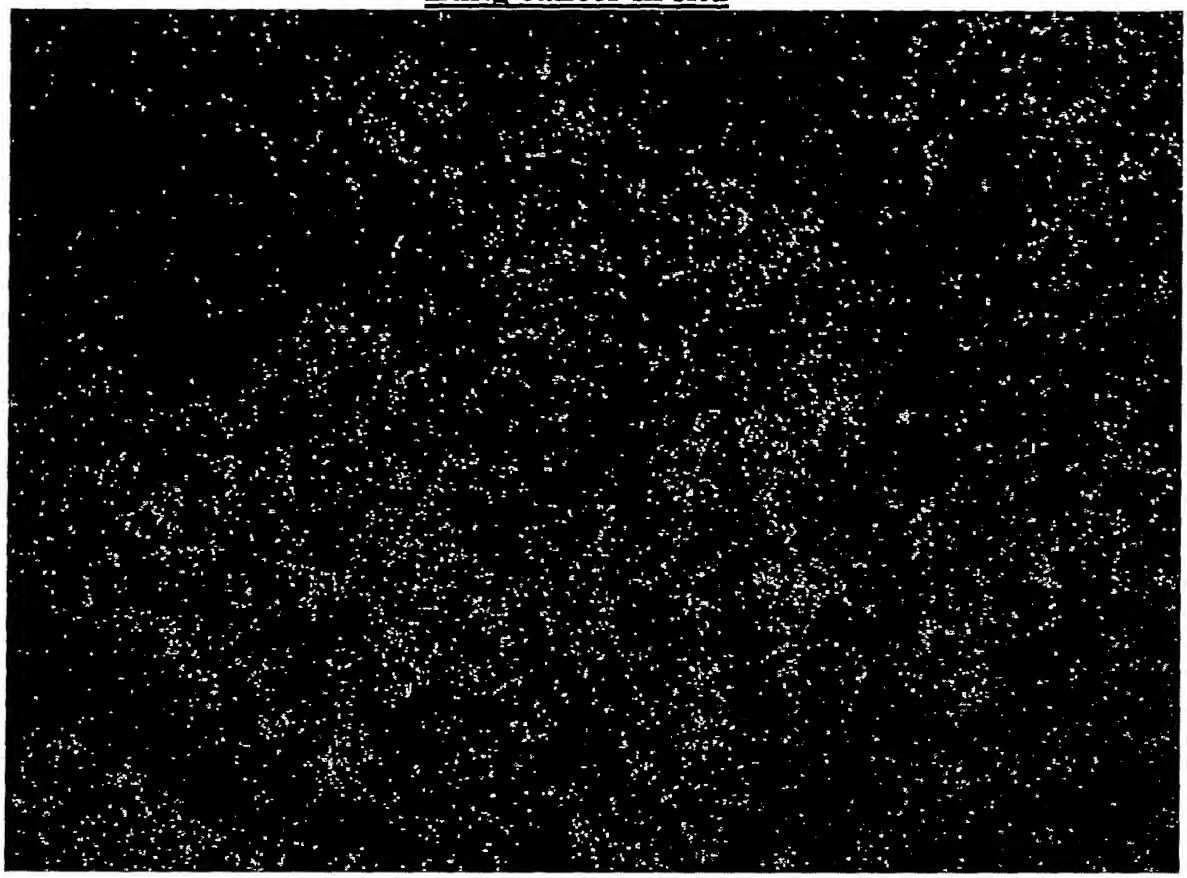
**Lung cancer in situ**



# FIGURE 9B



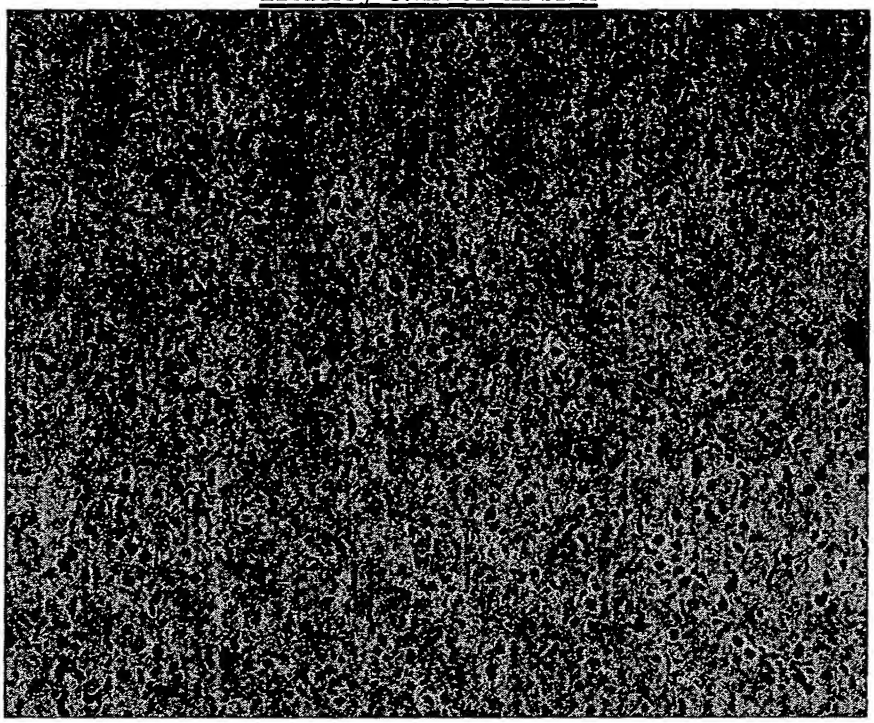
**Lung cancer in situ**



# FIGURE 10A



**Kidney cancer in situ**



# FIGURE 10B



**Kidney cancer in situ**

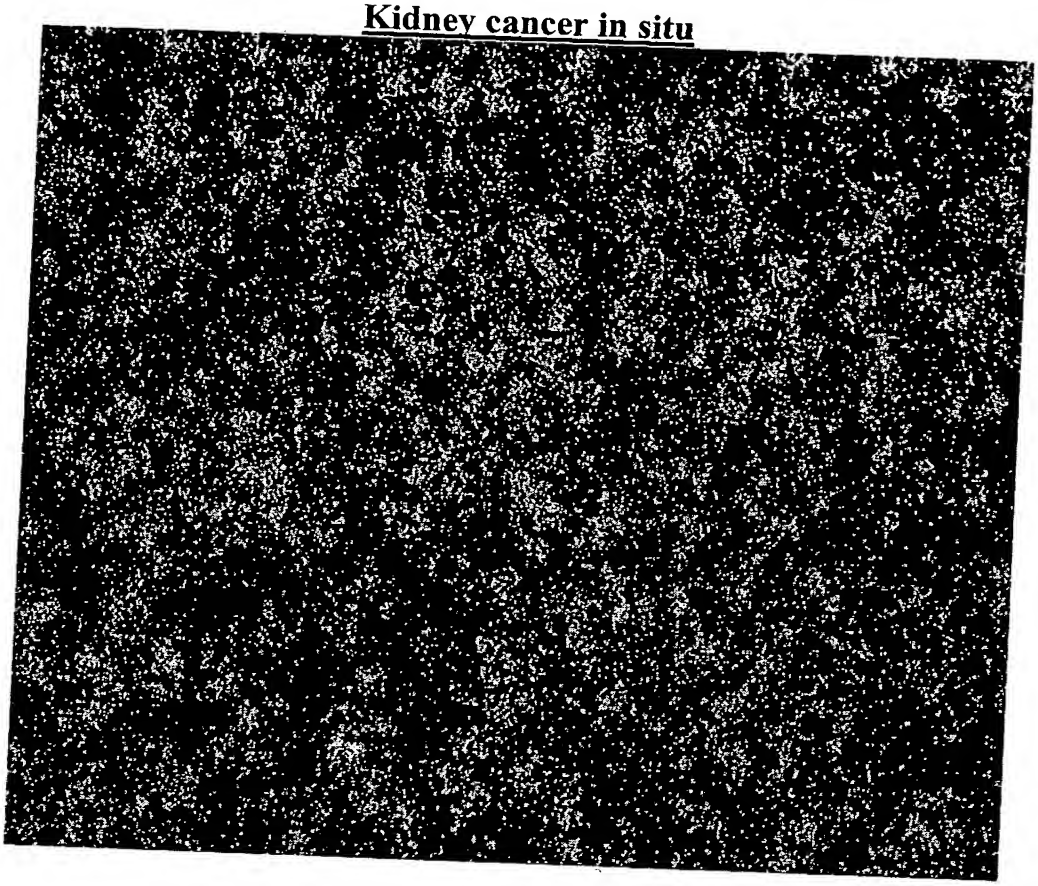


**FIGURE 11A**



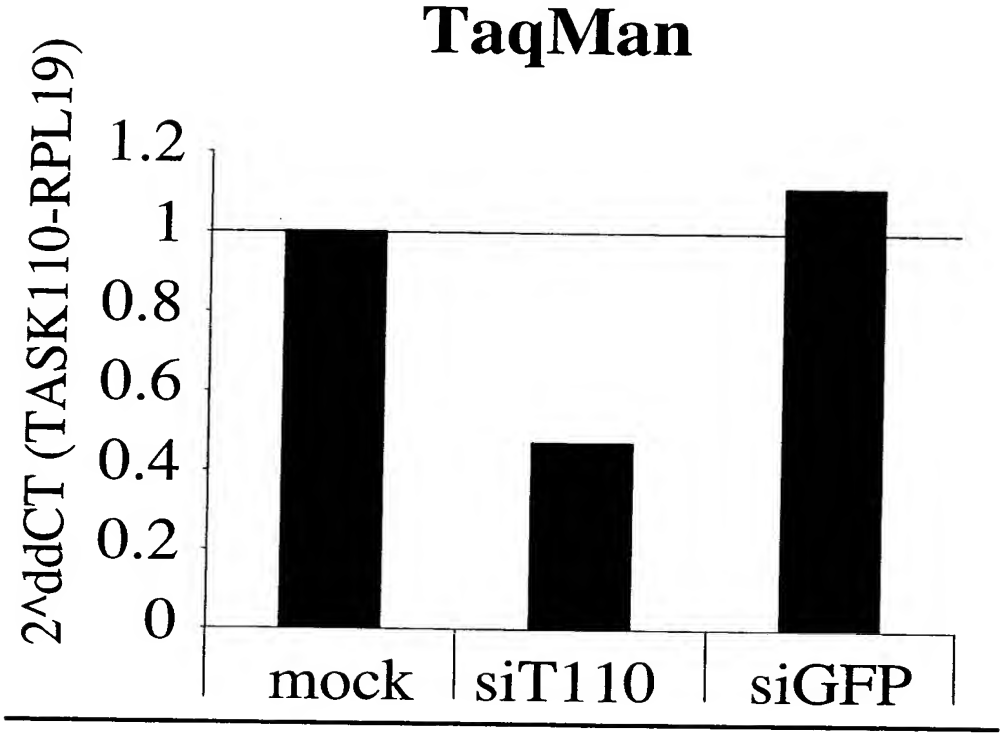

TaqMan
2^ddCT (TASK110-RPL19)
1.2
1
0.8
0.6
0.4
0.2
0
mock
siT110
siGFP

**FIGURE 11B**



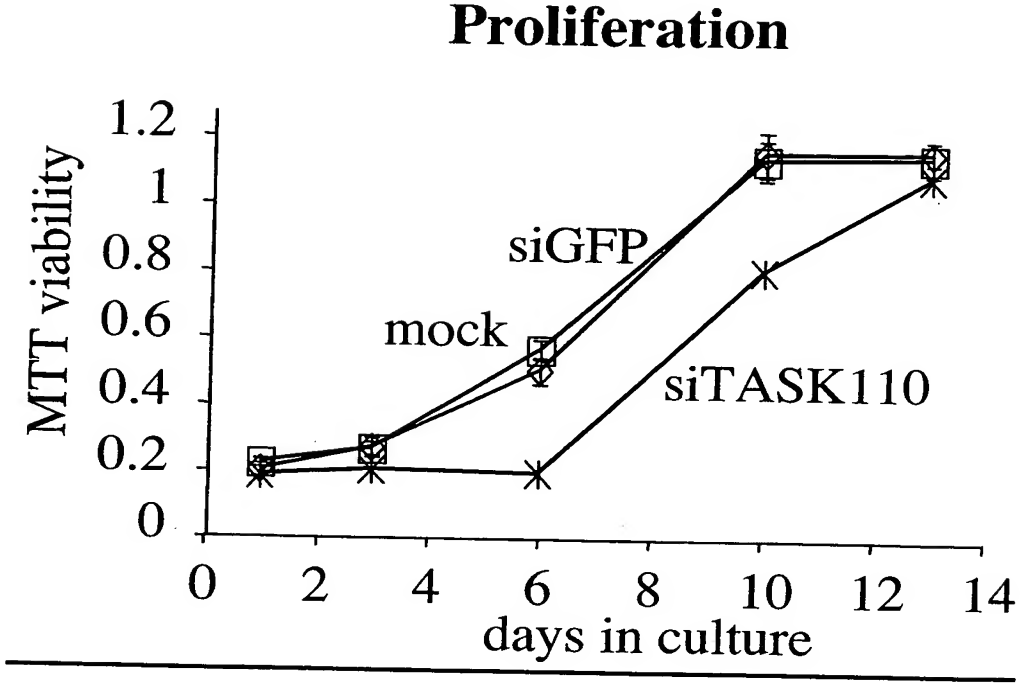
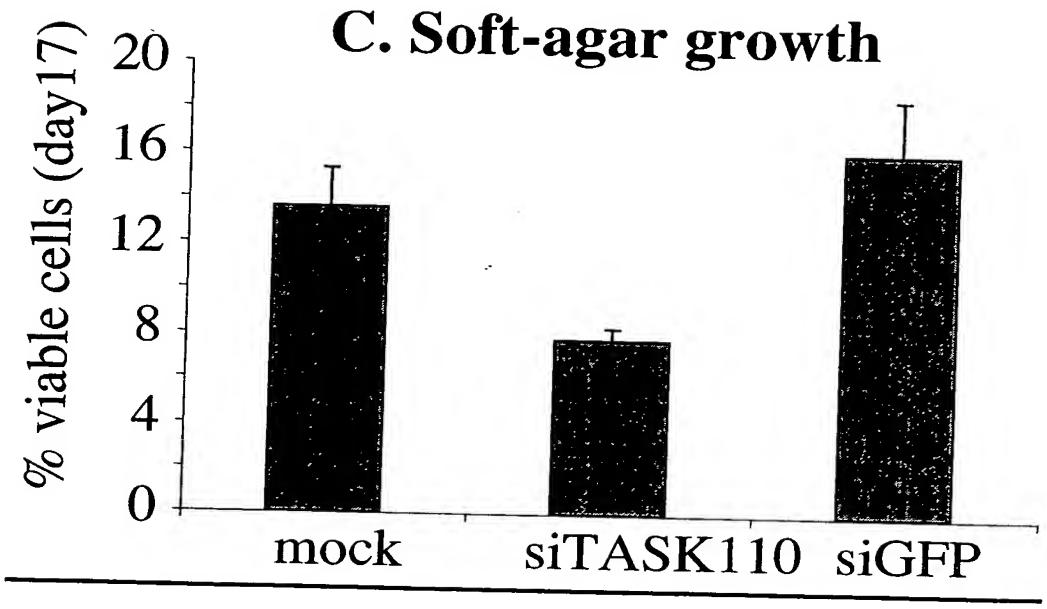

Proliferation
MTT viability
1.2
1
0.8
0.6
0.4
0.2
0
siGFP
mock
siTASK110
0
2
4
6
8
10
12
14
days in culture

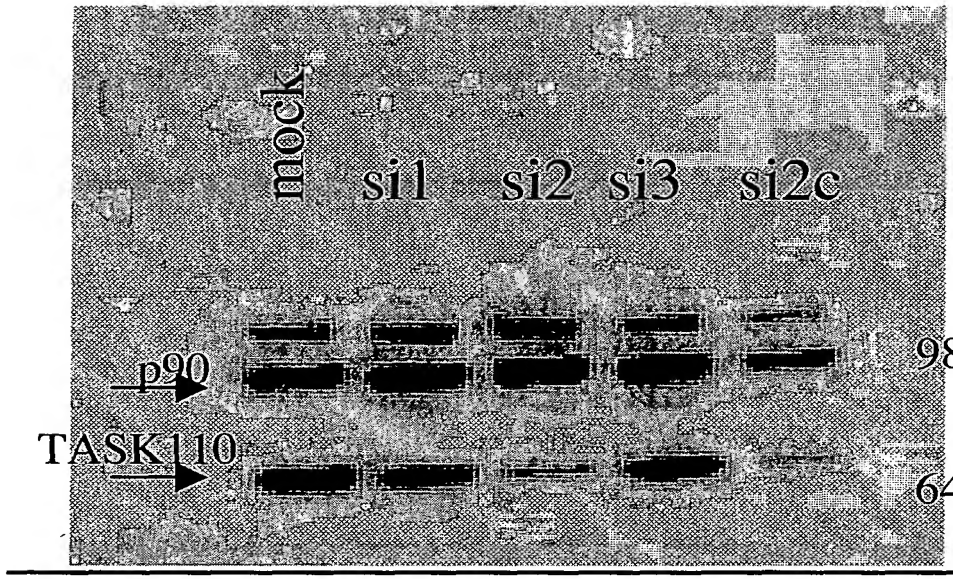
FIGURE 11C




C. Soft-agar growth
% viable cells (day17)
20
16
12
8
4
0
mock
siTASK110
siGFP

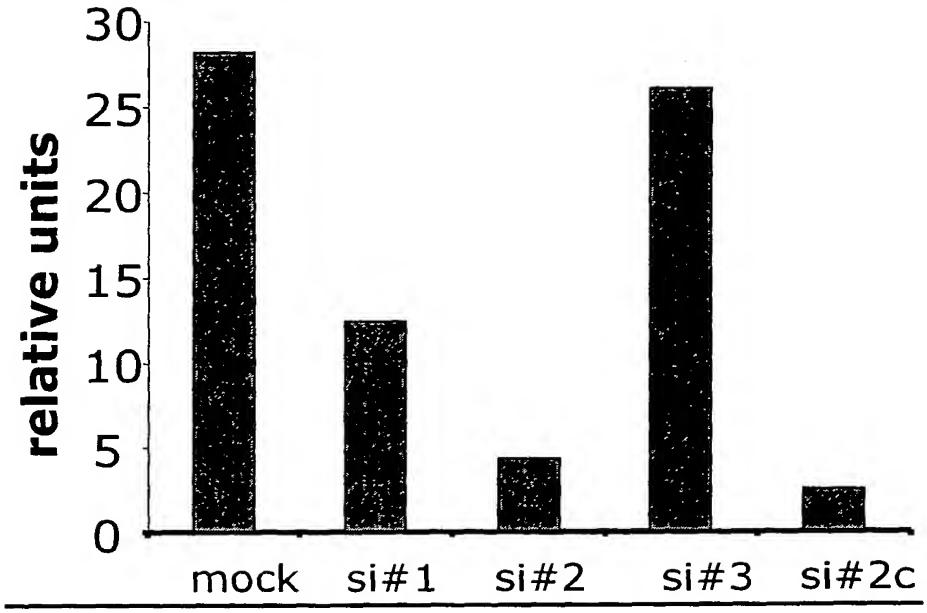
# FIGURE 11D





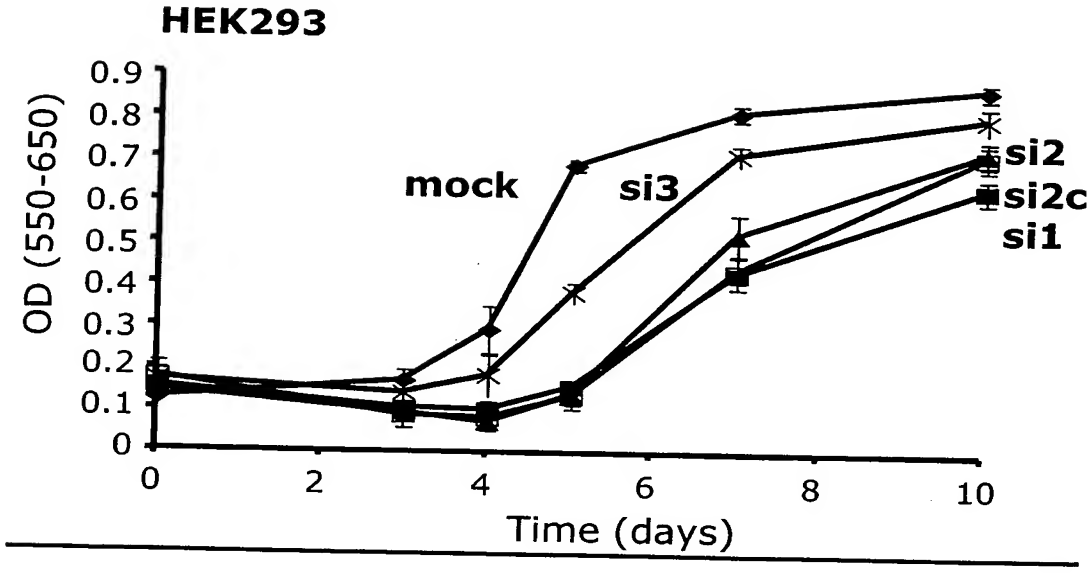
# FIGURE 11E





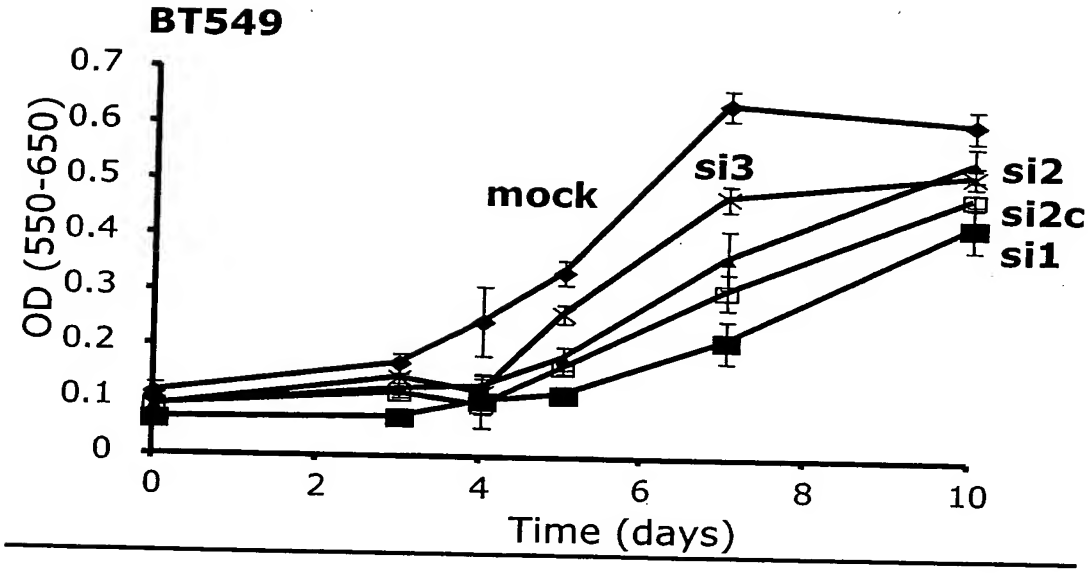
# FIGURE 11F




HEK293
OD (550-650)
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
Time (days)
mock
si3
si2
si2c
si1

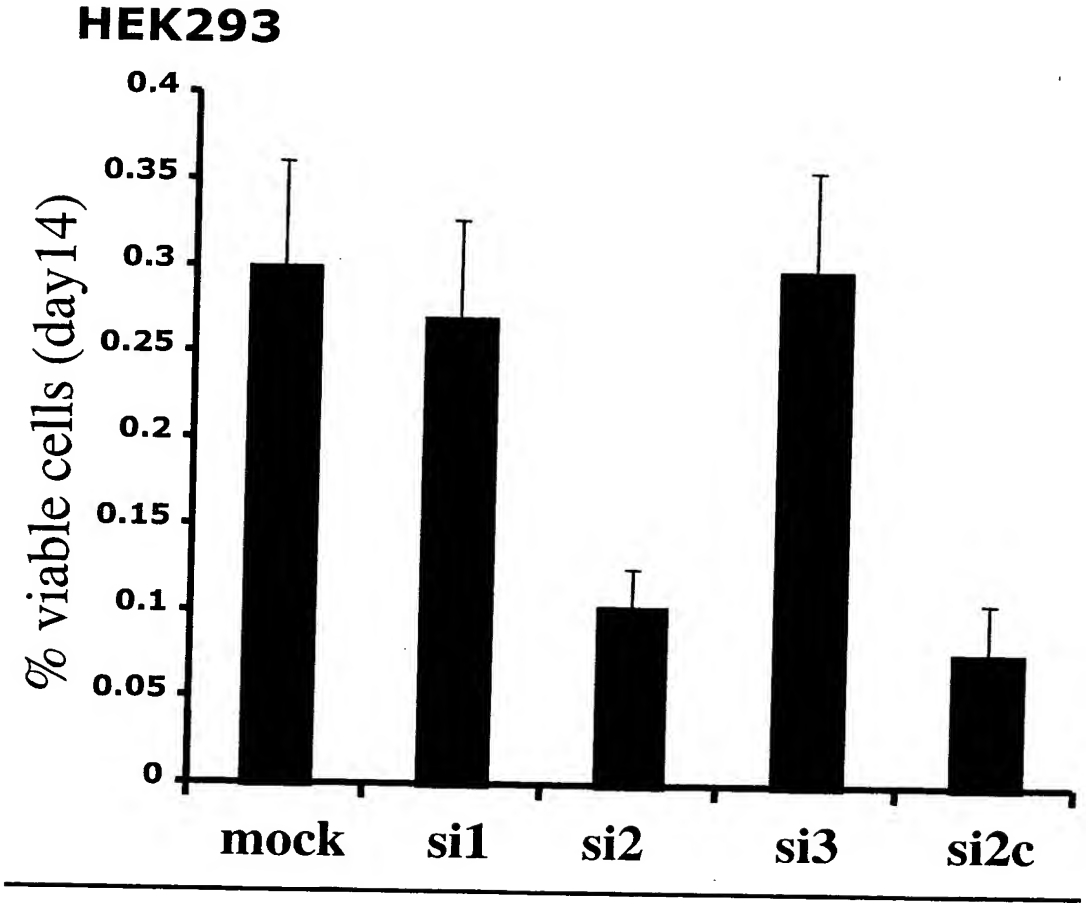
# FIGURE 11G




BT549
OD (550-650)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
Time (days)
mock
si3
si2
si2c
si1

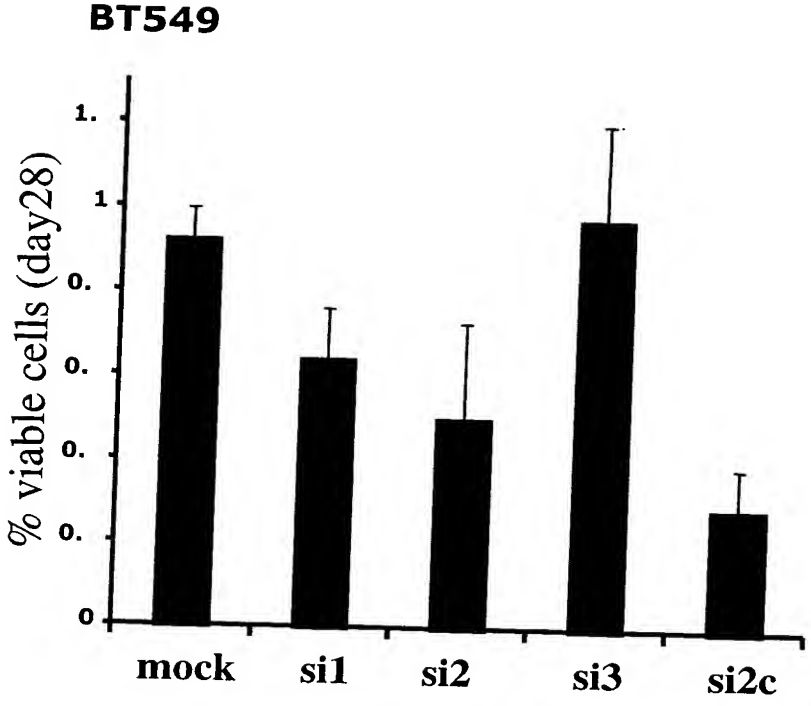
# FIGURE 11H




HEK293
% viable cells (day14)
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
mock
si1
si2
si3
si2c

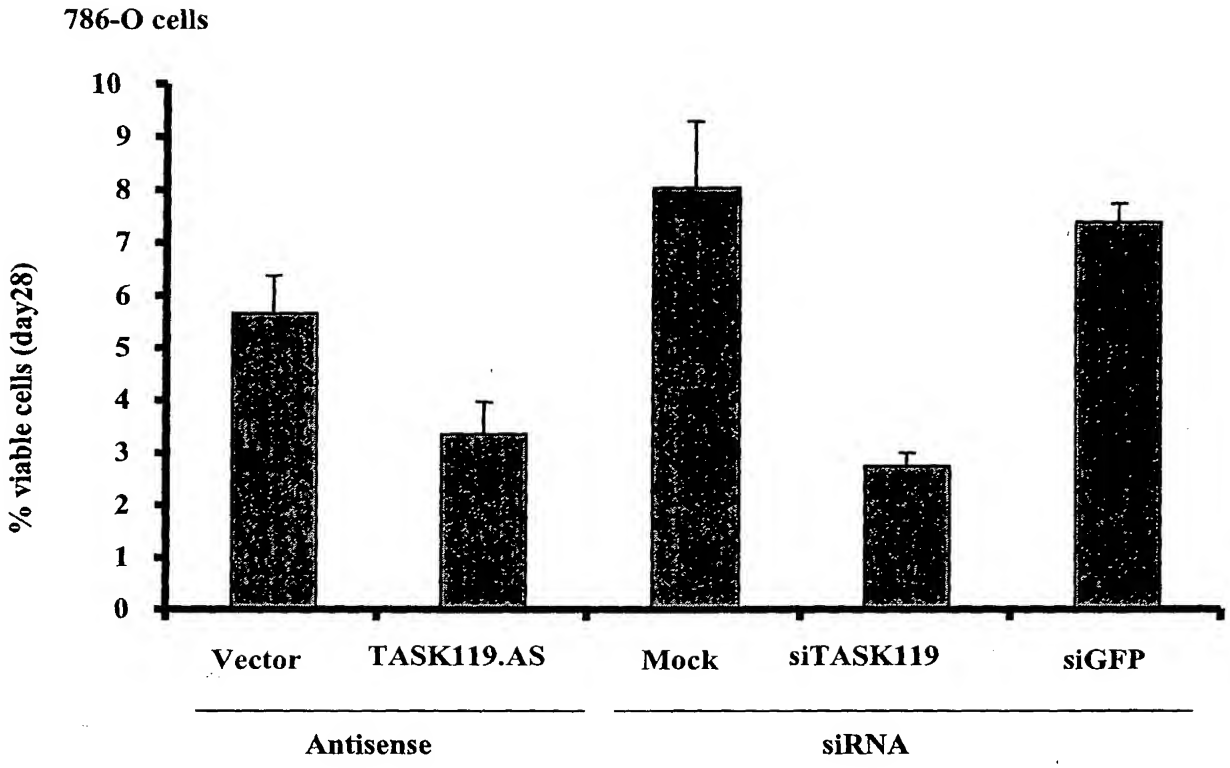
# FIGURE 11(I)





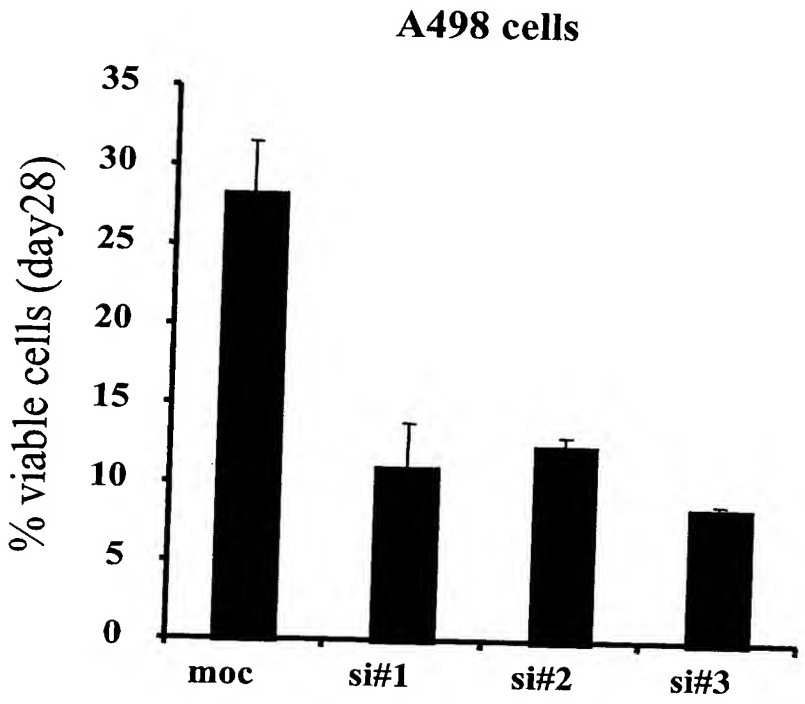
# FIGURE 12



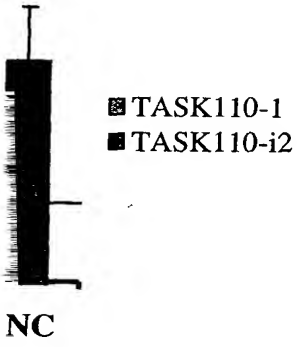

786-O cells
% viable cells (day28)
10
9
8
7
6
5
4
3
2
1
0
Vector
TASK119.AS
Mock
siTASK119
siGFP
Antisense
siRNA

# FIGURE 13



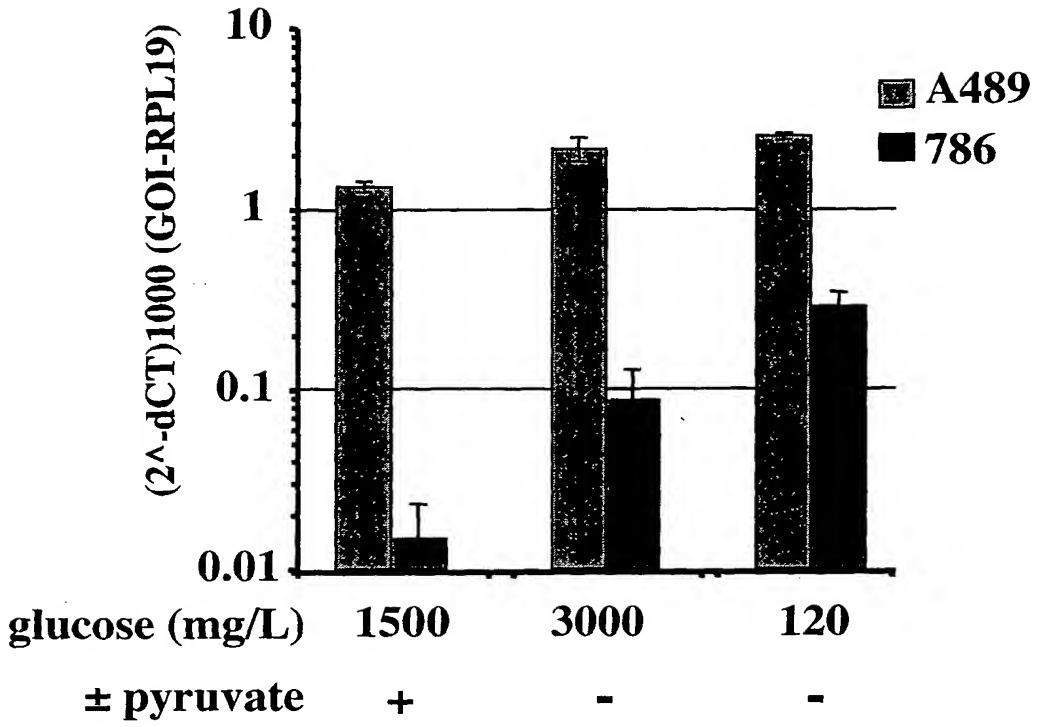

A498 cells
% viable cells (day28)
35
30
25
20
15
10
5
0
moc
si#1
si#2
si#3

› 4 control genes



# FIGURE 15




10
1
0.1
0.01
(2^-dCT)1000 (GOI-RPL19)
A489
786
glucose (mg/L)
1500
3000
120
± pyruvate
+
-
-